



SEQUENCE LISTING

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<120> MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
CONVERTASE WITH A UNIQUE CLEAVAGE SPECIFICITY

<130> IRCM

<140> PCT/CA99/01058
<141> 1999-11-04

<150> CA 2,249,648
<151> 1998-11-04

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<170> PatentIn Ver. 2.1

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tct tgg ttt ctg gat gcc ttc aac tat gcc atc cta aag aag atg gac	913		
Ser Trp Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp			
290	295	300	
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Val Leu Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe			
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gtt gac aag gtg tgg gaa tta aca gct aac aat gta att atg gtt tct	1009		
Val Asp Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser			
320	325	330	

gct att ggc aat gat gga cct ctc tat ggc act ctg aat aac cct gct		1057
Ala Ile Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala		
335	340	345
350		
gat cag atg gat gtg att gga gtg ggt ggc att gac ttt gaa gat aac		1105
Asp Gln Met Asp Val Ile Gly Val Gly Ile Asp Phe Glu Asp Asn		
355	360	365
atc gct cgc ttt tct tcc agg gga atg act acc tgg gaa tta cca gga		1153
Ile Ala Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly		
370	375	380
ggc tat ggt cgt gtg aag cct gac att gtc acc tat ggt gct gga gtg		1201
Gly Tyr Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val		
385	390	395
cgg ggt tcc ggt gtg aaa ggg ggc tgc cgt gca ctc tca ggg acc agt		1249
Arg Gly Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser		
400	405	410
gtc gct tcc cca gtg gtc gct ggg gcc gtc acc ttg tta gta agc aca		1297
Val Ala Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr		
415	420	425
430		
gta cag aag cgg gag ctg gtg aat cct gcc agt gtg aag caa gct ttg		1345
Val Gln Lys Arg Glu Leu Val Asn Pro Ala Ser Val Lys Gln Ala Leu		
435	440	445
ata gcg tca gcc cgg aga ctt cct ggg gtc aac atg ttc gag caa ggt		1393
Ile Ala Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly		
450	455	460
cat ggc aag ttg gat ctg ctg cga gct tat cag atc ctc agc agc tat		1441
His Gly Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Ser Ser Tyr		
465	470	475
aaa ccg cag gca agc ctg agt cct agc tac atc gac ctg act gag tgt		1489
Lys Pro Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys		
480	485	490
ccc tac atg tgg ccc tac tgc tcc cag cct atc tac tat gga gga atg		1537
Pro Tyr Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met		
495	500	505
510		
cca aca atc gtt aat gtc acc atc ctc aat ggc atg ggc gtc aca gga		1585
Pro Thr Ile Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly		
515	520	525

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Arg Ile Val Asp Lys Pro Glu Trp Arg Pro Tyr Leu Pro Gln Asn Gly			
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Asp Asn Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp			
545	550	555	
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Ser Gly Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser			
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Trp Glu Gly Ile Ala Gln Gly His Ile Met Ile Thr Val Ala Ser Pro			
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Ala Glu Thr Glu Leu His Ser Gly Ala Glu His Thr Ser Thr Val Lys			
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Leu Pro Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg			
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gtc ctc tgg gac cag tac cac aac ctc cgc tac cca cct ggc tac ttc			1921
Val Leu Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe			
625	630	635	
ccc agg gac aac ttg cggt atg aag aat gac cct tta gac tgg aat ggc			1969
Pro Arg Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly			
640	645	650	
gac cac gtc cac acc aac ttc agg gac atg tac cag cat ctg cgc agc			2017
Asp His Val His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser			
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Met Gly Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp			
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Ala Thr Gln Tyr Gly Thr Leu Leu Val Asp Ser Glu Glu Glu Tyr			
690	695	700	
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Phe Pro Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu			
705	710	715	

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Met Gly Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Val Leu Ala Asn	
770 775 780	
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His Asp Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu	
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Asp Gly Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val	
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Ala Pro Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys	
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Cys Pro His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala			
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Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
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Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
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Glu Val Glu Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
85 90 95
Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
100 105 110
Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
115 120 125
Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asn Pro Ile
130 135 140
Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
145 150 155 160

Pro Leu Lys Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
165 170 175

Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
180 185 190

Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr
195 200 205

Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
210 215 220

His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
225 230 235 240

Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
245 250 255

Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
260 265 270

His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
275 280 285

Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu
290 295 300

Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
305 310 315 320

Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile
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Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
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Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu
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Thr Glu Leu His Ser Gly Ala Glu His Thr Ser Thr Val Lys Leu Pro
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Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu
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Gln Tyr Gly Thr Leu Leu Leu Val Asp Ser Glu Glu Glu Tyr Phe Pro
690 695 700

Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu
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Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys
725 730 735

Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly
740 745 750

Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly
755 760 765

Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Val Leu Ala Asn His Asp
770 775 780

Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly
785 790 795 800

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Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
850 855 860

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His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
885 890 895

Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
900 905 910

Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
915 920 925

His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
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Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
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980 985 990

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995 1000 1005

Gly Ala Met Val Ala Leu Ala Phe Phe Val Val Gln Ile Ser Lys Ala
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Ile Pro Arg Gln Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln			
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Leu Ser Glu Lys His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn			
225	230	235	
tgg acc aac gag cga acg ctg gac gat ggg ttg ggc cat ggc aca ttc			1252
Trp Thr Asn Glu Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe			
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Ile Asp Val Leu Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His			
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Pro Phe Val Asp Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met			
320	325	330	
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Val Ser Ala Ile Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn			
335	340	345	
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Pro Ala Asp Gln Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu			
350	355	360	

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Asp Asn Ile Ala Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu			
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385	390	395	
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Thr Ser Val Ala Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val			
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Ser Thr Val Gln Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln			
430	435	440	
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Ala Leu Ile Ala Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu			
445	450	455	460
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495	500	505	
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Asn Gly Asp Asn Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp			
545	550	555	

cct tgg tcg ggc tac ctg gcc atc tcc att tct gtg acc aag aaa gcg			2212
Pro Trp Ser Gly Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala			
560	565	570	
gct tcc tgg gaa ggc att gct cag ggc cat gtc atg atc act gtg gct			2260
Ala Ser Trp Glu Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala			
575	580	585	
tcc cca gca gag aca gag tca aaa aat ggt gca gaa cag act tca aca			2308
Ser Pro Ala Glu Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr			
590	595	600	
gta aag ctc ccc att aag gtg aag ata att cct act ccc ccg cga agc			2356
Val Lys Leu Pro Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser			
605	610	615	620
aag aga gtt ctc tgg gat cag tac cac aac ctc cgc tat cca cct ggc			2404
Lys Arg Val Leu Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly			
625	630	635	
tat ttc ccc agg gat aat tta agg atg aag aat gac cct tta gac tgg			2452
Tyr Phe Pro Arg Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp			
640	645	650	
aat ggt gat cac atc cac acc aat ttc agg gat atg tac cag cat ctg			2500
Asn Gly Asp His Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu			
655	660	665	
aga agc atg ggc tac ttt gta gag gtc ctc ggg gcc ccc ttc acg tgt			2548
Arg Ser Met Gly Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys			
670	675	680	
ttt gat gcc agt cag tat ggc act ttg ctg atg gtg gac agt gag gag			2596
Phe Asp Ala Ser Gln Tyr Gly Thr Leu Leu Met Val Asp Ser Glu Glu			
685	690	695	700
gag tac ttc cct gaa gag atc gcc aag ctc cgg agg gac gtg gac aac			2644
Glu Tyr Phe Pro Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn			
705	710	715	
ggc ctc tcg ctc gtc atc ttc agt gac tgg tac aac act tct gtt atg			2692
Gly Leu Ser Leu Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met			
720	725	730	
aga aaa gtg aag ttt tat gat gaa aac aca agg cag tgg tgg atg ccg			2740
Arg Lys Val Lys Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro			
735	740	745	

gat acc gga gga gct aac atc cca gct ctg aat gag ctg ctg tct gtg			2788
Asp Thr Gly Gly Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val			
750	755	760	
tgg aac atg ggg ttc agc gat ggc ctg tat gaa ggg gag ttc acc ctg			2836
Trp Asn Met Gly Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu			
765	770	775	780
gcc aac cat gac atg tat tat gcg tca ggg tgc agc atc gcg aag ttt			2884
Ala Asn His Asp Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe			
785	790	795	
cca gaa gat ggc gtc gtg ata aca cag act ttc aag gac caa gga ttg			2932
Pro Glu Asp Gly Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu			
800	805	810	
gag gtt tta aag cag gaa aca gca gtt gtt gaa aac gtc ccc att ttg			2980
Glu Val Leu Lys Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu			
815	820	825	
gga ctt tat cag att cca gct gag ggt gga ggc cgg att gta ctg tat			3028
Gly Leu Tyr Gln Ile Pro Ala Glu Gly Gly Arg Ile Val Leu Tyr			
830	835	840	
ggg gac tcc aat tgc ttg gat gac agt cac cga cag aag gac tgc ttt			3076
Gly Asp Ser Asn Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe			
845	850	855	860
tgg ctt ctg gat gcc ctc ctc cag tac aca tcg tat ggg gtg aca ccg			3124
Trp Leu Leu Asp Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro			
865	870	875	
cct agc ctc agt cac tct ggg aac cgc cag cgc cct ccc agt gga gca			3172
Pro Ser Leu Ser His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala			
880	885	890	
ggc tca gtc act cca gag agg atg gaa gga aac cat ctt cat cgg tac			3220
Gly Ser Val Thr Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr			
895	900	905	
tcc aag gtt ctg gag gcc cat ttg gga gac cca aaa cct cgg cct cta			3268
Ser Lys Val Leu Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu			
910	915	920	
cca gcc tgt cca cgc ttg tct tgg gcc aag cca cag cct tta aac gag			3316
Pro Ala Cys Pro Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu			
925	930	935	940

acg gcg ccc agt aac ctt tgg aaa cat cag aag cta ctc tcc att gac	3364		
Thr Ala Pro Ser Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp			
945	950	955	
ctg gac aag gtg gtg tta ccc aac ttt cga tcg aat cgc cct caa gtg	3412		
Leu Asp Lys Val Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val			
960	965	970	
agg ccc ttg tcc cct gga gag agc ggc gcc tgg gac att cct gga ggg	3460		
Arg Pro Leu Ser Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly			
975	980	985	
atc atg cct ggc cgc tac aac cag gag gtg ggc cag acc att cct gtc	3508		
Ile Met Pro Gly Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val			
990	995	1000	
ttt gcc ttc ctg gga gcc atg gtg gtc ctg gcc ttc ttt gtg gta caa	3556		
Phe Ala Phe Leu Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln			
1005	1010	1015	1020
atc aac aag gcc aag agc agg ccg aag cgg agg aag ccc agg gtg aag	3604		
Ile Asn Lys Ala Lys Ser Arg Pro Lys Arg Arg Lys Pro Arg Val Lys			
1025	1030	1035	
cgc ccg cag ctc atg cag cag gtt cac ccg cca aag acc cct tcg gtg	3652		
Arg Pro Gln Leu Met Gln Gln Val His Pro Pro Lys Thr Pro Ser Val			
1040	1045	1050	
tgaccggcag cctggctgac cgtgagggcc agagagagcc ttcacggacg gcgctggtgg 3712			
gtgagccgag ctgtggtggc ggctggttta aaaggatcc agtttccagc tgcaggttt 3772			
tttagagtctg ttctacatgg gcctgccctc ctgtgatggg cagaggctcc tggcacatcg 3832			
agaagattcc tgtggatccc gtcaggaggg acttagtggc tctgccgcca gtgagacttc 3892			
ccgcccggcag ctgtgcgcac caaagactcg ggagaactgg aaaggctgtc tgggtcttc 3952			
tgactgcagg ggaaggatgt actttccaaa caaatgatac aaccctgacc aagctaaaag 4012			
acgcttgtta aaggctattt tctatattta ttgttggaa aagtcaactt aaagacttgt 4072			
gctatggaa agcaaagcta tttttttgt cagtggatg cagttttttt actattccat 4132			
catgaggaac aacatagatt ccatgatctt ttatgaca gtacagactg agatggaa 4192			
gaaacatgca caaatctgta aaacatagac ctgcgttta ttttgtaag tatcacctgc 4252			

caccatgttt tgtaatttga ggtcttgatt tcaccattgtt cggtgaagaa aattttcaat 4312

aaatatgtat tacccgtctg aagctt 4338

<210> 6

<211> 1052

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Leu Val Asn Ile Trp Leu Leu Leu Val Val Leu Leu Cys
1 5 10 15

Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys Ser Phe Glu Lys
20 25 30

Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
35 40 45

Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
50 55 60

Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
65 70 75 80

Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
85 90 95

Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
100 105 110

Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
115 120 125

Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr
130 135 140

Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
145 150 155 160

Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
165 170 175

Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
180 185 190

Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr

195 200 205
Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
210 215 220
His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
225 230 235 240
Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
245 250 255
Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
260 265 270
His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
275 280 285
Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Ile Asp Val Leu
290 295 300
Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
305 310 315 320
Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile
325 330 335
Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln
340 345 350
Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala
355 360 365
Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr
370 375 380
Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly
385 390 395 400
Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
405 410 415
Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln
420 425 430
Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln Ala Leu Ile Ala
435 440 445
Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly

450 455 460
Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Asn Ser Tyr Lys Pro
465 470 475 480
Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr
485 490 495
Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr
500 505 510
Val Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile
515 520 525
Val Asp Lys Pro Asp Trp Gln Pro Tyr Leu Pro Gln Asn Gly Asp Asn
530 535 540
Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly
545 550 555 560
Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu
565 570 575
Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala Ser Pro Ala Glu
580 585 590
Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr Val Lys Leu Pro
595 600 605
Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu
610 615 620
Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg
625 630 635 640
Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His
645 650 655
Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly
660 665 670
Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp Ala Ser
675 680 685
Gln Tyr Gly Thr Leu Leu Met Val Asp Ser Glu Glu Glu Tyr Phe Pro
690 695 700
Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu

705 710 715 720

Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys
725 730 735

Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly
740 745 750

Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly
755 760 765

Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu Ala Asn His Asp
770 775 780

Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly
785 790 795 800

Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val Leu Lys
805 810 815

Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu Gly Leu Tyr Gln
820 825 830

Ile Pro Ala Glu Gly Gly Arg Ile Val Leu Tyr Gly Asp Ser Asn
835 840 845

Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
850 855 860

Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
865 870 875 880

His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Ser Val Thr
885 890 895

Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
900 905 910

Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
915 920 925

Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
930 935 940

Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
945 950 955 960

Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser

965 970 975
Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
980 985 990
Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
995 1000 1005
Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln Ile Asn Lys Ala
1010 1015 1020
Lys Ser Arg Pro Lys Arg Arg Lys Pro Arg Val Lys Arg Pro Gln Leu
025 1030 1035 1040
Met Gln Gln Val His Pro Pro Lys Thr Pro Ser Val
1045 1050

<210> 7

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>

<221> MOD_RES

<222> (4)...(6)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (7)

<223> Xaa represents an acidic amino acid.

<400> 7
Arg Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (3)
<223> Xaa represents an alkyl or an aromatic hydrophobic
amino acid.

<220>
<221> MOD_RES
<222> (4)
<223> Xaa represents Lys, Leu, Phe or Thr.

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (7)
<223> Xaa represents an acidic amino acid.

<400> 8
Arg Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (3)
<223> Xaa represents an alkyl or an aromatic hydrophobic acid.

<220>
<221> MOD_RES
<222> (4)..(7)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (8)
<223> Xaa represents an acidic amino acid.

<400> 9
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (3)
<223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>
<221> MOD_RES
<222> (4)
<223> Xaa represents Lys, Leu, Phe or Thr.

<220>
<221> MOD_RES
<222> (5)..(7)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (8)
<223> Xaa represents an acidic amino acid.

<400> 10
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (3)
<223> Xaa is an alkyl or an aromatic hydrophobic amino acid.

<220>
<221> MOD_RES
<222> (4)..(8)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (9)

<223> Xaa represents an acidic amino acid.

<400> 11

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 12

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic
amino acid.

<220>

<221> MOD_RES

<222> (4)

<223> Xaa represents Lys, Leu, Phe or Thr.

<220>

<221> MOD_RES

<222> (5)..(8)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (9)

<223> Xaa represents an acid amino acid.

<400> 12

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 13

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 13
Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp
1 5 10

<210> 14
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (1)
<223> Xaa represents orthoaminobenzoic acid.

<220>
<221> MOD_RES
<222> (13)
<223> Xaa represents 3-nitrotyrosine.

<400> 14
Xaa Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa
1 5 10

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<220>
<221> modified_base
<222> (3)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base
<222> (21)
<223> i

<400> 15
ggncayggna cnywykkngc ngg

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<220>
<221> modified_base
<222> (3)
<223> i

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

23

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<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> modified_base
<222> (15)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base
<222> (21)
<223> i

<220>
<221> modified_base
<222> (24)
<223> i

<220>
<221> modified_base
<222> (29)
<223> i

<400> 16
ccngynacnw snggnswngc nacnswgtn c
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31

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<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa represents histidine or phenylalanine.

<220>
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<221> MOD_RES
<222> (6)
<223> Xaa represents valine or cysteine.

<400> 17
Gly His Gly Thr Xaa Xaa Ala Gly
1 5

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (4)
<223> Xaa represents valine or methionine.

<220>
<221> MOD_RES
<222> (6)
<223> Xaa represents threonine or serine.

<220>
<221> MOD_RES
<222> (8)
<223> Xaa represents histidine or valine.

<220>
<221> MOD_RES
<222> (10)
<223> Xaa represents alanine or threonine.

<400> 18
Gly Thr Ser Xaa Ala Xaa Pro Xaa Val Xaa Gly
1 5 10

<210> 19
<211> 28
<212> DNA
<213> Homo sapiens

<400> 19

ggatccgaag aaacatctgg gcgacaga

28

<210> 20
<211> 24
<212> DNA
<213> Homo sapiens

<400> 20
ctcgagggct ctcagccgtg tgct

24

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21
gaggaagaga caggataaa c

21

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 22
gggatatgct tagcattgac

20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 23

agcccttatta cctgaacctg

20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 24
gaatctgaaa gaactccccc

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 25
ttccgagatt ccatcctacg

20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 26
tgcagctcag caggctatg

20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 27
tctcctccaa cctcaaccac

20

<210> 28
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 28
ccagcctgtc atcctcaata tc

22

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 29
ggagccatgg attgcacttt c

21

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 30
aggagctcaa tgtggcagga

20

<210> 31
<211> 27

<212> DNA
<213> Homo sapiens

<400> 31
gtgaccatga agcttgtcaa catctgg

27

<210> 32
<211> 26
<212> DNA
<213> Homo sapiens

<400> 32
acactggtcc ctgagagggc ccggca

26

<210> 33
<211> 21
<212> DNA
<213> Homo sapiens

<400> 33
attgacacctgg acaaggtggt g

21

<210> 34
<211> 57
<212> DNA
<213> Homo sapiens

<400> 34
ggatcctcta gatcagtgggt ggtgggtggtg gtggtgctcc tggttgttagc ggccagg

57

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
ctcgagggag aggctggctc ttcg

24

<210> 36
<211> 28
<212> DNA
<213> Homo sapiens

<400> 36
ctcgagtgta tggcaacct ggcgcgaa

28

<210> 37
<211> 14
<212> PRT
<213> Homo sapiens

<400> 37
Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe
1 5 10

<210> 38
<211> 27
<212> PRT
<213> Homo sapiens

<400> 38
Gly Gly Ala His Asp Ser Asp Gln His Pro His Ser Gly Ser Gly Arg
1 5 10 15
Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly
20 25

<210> 39
<211> 18
<212> PRT
<213> Homo sapiens

<400> 39
Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile
1 5 10 15
Pro Arg

<210> 40
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 40

Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Leu
1 5 10 15

Glu

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 41

Ser Arg Arg Leu Leu Arg Ala Leu Glu
1 5

<210> 42

<211> 17

<212> PRT

<213> Homo sapiens

<400> 42

Trp Gln Ser Ser Arg Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser
1 5 10 15

Gly

<210> 43

<211> 15

<212> PRT

<213> Homo sapiens

<400> 43

Arg Ala Ile Pro Arg Gln Val Ala Gln Thr Leu Gln Ala Asp Val
1 5 10 15

<210> 44

<211> 9

<212> PRT

<213> Homo sapiens

<400> 44
Pro Gln Arg Lys Val Phe Arg Ser Leu
1 5

<210> 45
<211> 15
<212> PRT
<213> Homo sapiens

<400> 45
Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp
1 5 10 15

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (1)
<223> Xaa represents orthoaminobenzoic acid.

<220>
<221> MOD_RES
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<223> Xaa represents 3-nitrotyrosine.

<220>
<223> Description of Artificial Sequence: Peptide

<400> 46
Xaa Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa Ala
1 5 10

<210> 47
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
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<223> Xaa represents orthoaminobenzoic acid.

<220>
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<223> Xaa represent 3-nitrotyrosine.

<220>
<223> Description of Artificial Sequence: Peptide

<400> 47
Xaa Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa Ala
1 5 10

<210> 48
<211> 16
<212> PRT
<213> Homo sapiens

<400> 48
Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His
1 5 10 15

<210> 49
<211> 16
<212> PRT
<213> Rattus sp.

<400> 49
Lys Ala Gly Ser Arg Gly Leu Thr Thr Ser Leu Ala Asp Thr Phe
1 5 10 15

<210> 50
<211> 16
<212> PRT
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<400> 50
Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln Val Ala
1 5 10 15

<210> 51
<211> 16
<212> PRT
<213> Homo sapiens

<400> 51
Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr Val
1 5 10 15

<210> 52
<211> 16
<212> PRT
<213> Homo sapiens

<400> 52
Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp
1 5 10 15

<210> 53
<211> 16
<212> PRT
<213> Homo sapiens

<400> 53
Val Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Lys Tyr Ala Glu
1 5 10 15

<210> 54
<211> 16
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<400> 54
Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly
1 5 10 15

<210> 55
<211> 16
<212> PRT
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<400> 55
His Ser Pro Gly Arg Asn Val Leu Gly Thr Glu Ser Arg Asp Gly Pro
1 5 10 15

<210> 56
<211> 16

<212> PRT

<213> Rattus sp.

<400> 56

Ala Ser Val Gly Arg Leu Ala Leu Ser Gln Glu Glu Pro Ala Pro Leu
1 5 10 15

<210> 57

<211> 16

<212> PRT

<213> Homo sapiens

<400> 57

Arg Ile Ser Asp Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg
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<210> 58

<211> 16

<212> PRT

<213> Rattus sp.

<400> 58

Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser Leu Ala Ala Ala Thr
1 5 10 15

<210> 59

<211> 16

<212> PRT

<213> Bovis sp.

<400> 59

Leu Leu Lys Glu Leu Gln Asp Leu Ala Leu Gln Gly Ala Lys Glu Arg
1 5 10 15

<210> 60

<211> 16

<212> PRT

<213> Bovis sp.

<400> 60

Met Ala Arg Ala Pro Gln Val Leu Phe Arg Gly Gly Lys Ser Gly Glu
1 5 10 15

<210> 61
<211> 16
<212> PRT
<213> Bovis sp.

<400> 61
Glu Leu Glu Asn Leu Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala
1 5 10 15

<210> 62
<211> 16
<212> PRT
<213> Bovis sp.

<400> 62
Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala Glu Lys Phe Ser Gly
1 5 10 15

<210> 63
<211> 16
<212> PRT
<213> Rattus sp.

<400> 63
Lys Ser Ser Phe Thr Asn Val Thr Ser Pro Val Val Leu Thr Asn Tyr
1 5 10 15

<210> 64
<211> 16
<212> PRT
<213> Rattus sp.

<400> 64
Lys Ser Gln Thr Pro Leu Val Thr Leu Phe Lys Asn Ala Ile Ile Lys
1 5 10 15

<210> 65
<211> 16
<212> PRT
<213> Rattus sp.

<400> 65
Ser Gln Thr Pro Leu Val Thr Leu Phe Lys Asn Ala Ile Ile Lys Asn
1 5 10 15

<210> 66
<211> 16
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<213> Rattus sp.

<400> 66
Gly Pro Ala Arg Glu Leu Leu Leu Arg Leu Val Gln Leu Ala Gly Thr
1 5 10 15

<210> 67
<211> 16
<212> PRT
<213> Homo sapiens

<400> 67
Leu Leu Arg Lys Lys Arg Thr Thr Ser Ala Glu Lys Asn Thr Cys Gln
1 5 10 15

<210> 68
<211> 16
<212> PRT
<213> Homo sapiens

<400> 68
Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser
1 5 10 15

<210> 69
<211> 16
<212> PRT
<213> Homo sapiens

<400> 69
Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser
1 5 10 15

<210> 70
<211> 16
<212> PRT
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<400> 70

Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10 15

<210> 71
<211> 16
<212> PRT
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<400> 71
Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val
1 5 10 15

<210> 72
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Peptide

<400> 72
Ser Ser Arg Arg Leu Leu Arg Ala Ile Glu
1 5 10

<210> 73
<211> 12
<212> PRT
<213> Homo sapiens

<400> 73
Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser
1 5 10

<210> 74
<211> 14
<212> PRT
<213> Artificial Sequence

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<223> Xaa represents orthoaminobenzoic acid.

<220>

<221> MOD_RES
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<223> Xaa represents 3-nitrotyrosine.

<220>
<223> Description of Artificial Sequence: Peptide

<400> 74
Xaa Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Xaa Ala
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<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
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<223> Xaa represents orthoaminobenzoic acid.

<220>
<221> MOD_RES
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<223> Xaa represents 3-nitrotyrosine.

<400> 75
Xaa Ser Arg Arg Leu Leu Arg Ala Leu Glu Xaa Ala
1 5 10

<210> 76
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<223> Xaa represents orthoaminobenzoic acid.

<220>
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<223> Xaa represents 3-nitrotyrosine.

<220>

<223> Description of Artificial Sequence: Peptide

<400> 76

Xaa Asn Gly Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Xaa Ala
1 5 10 15